

FIG. 1A

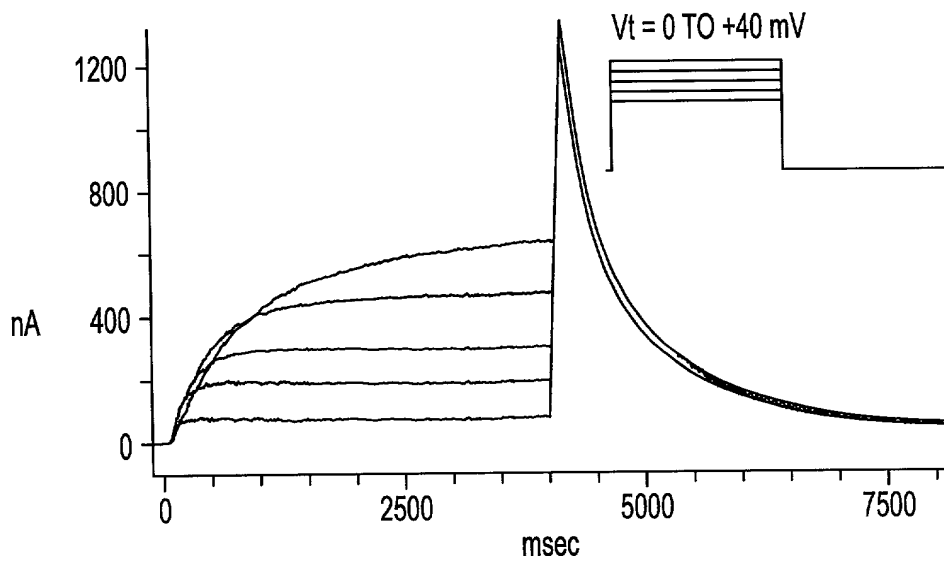


FIG. 1B

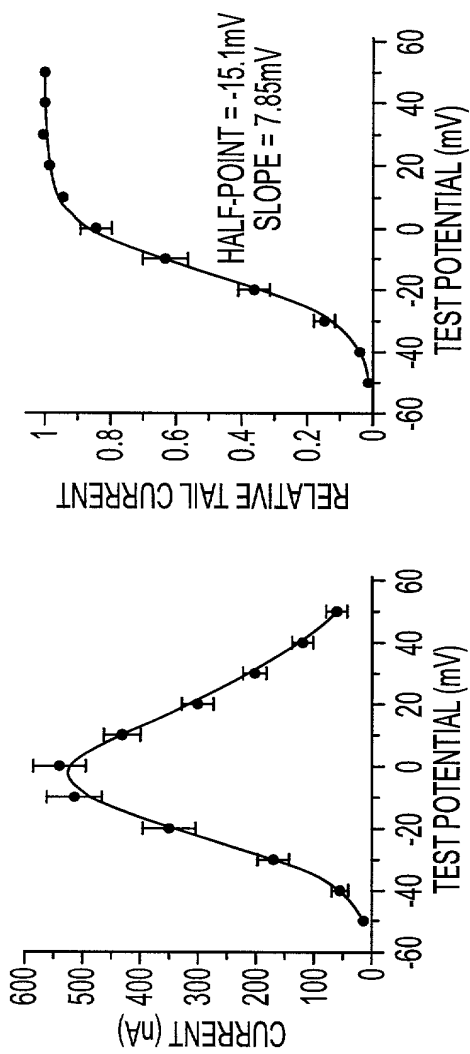


FIG. 1D

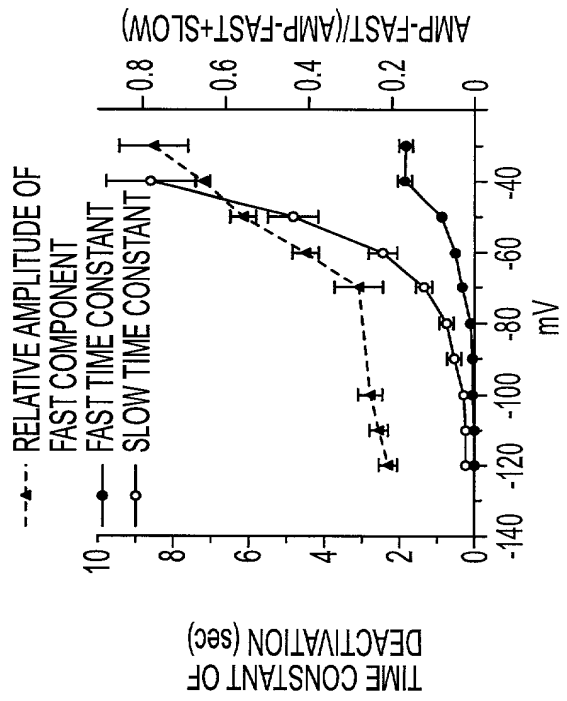
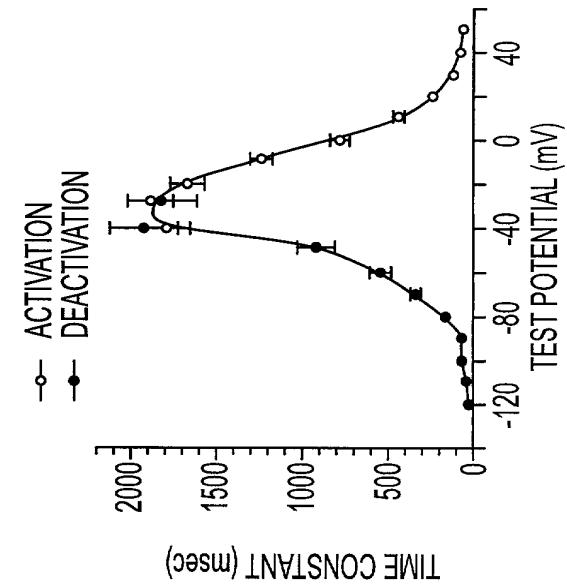
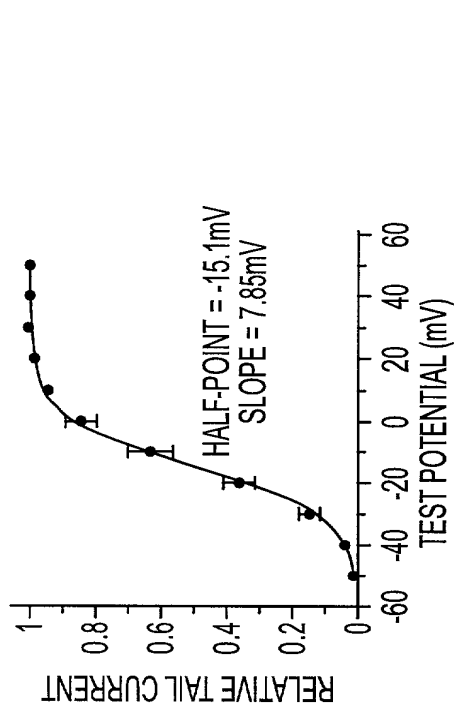


FIG. 2D

FIG. 2C

004121-56656260

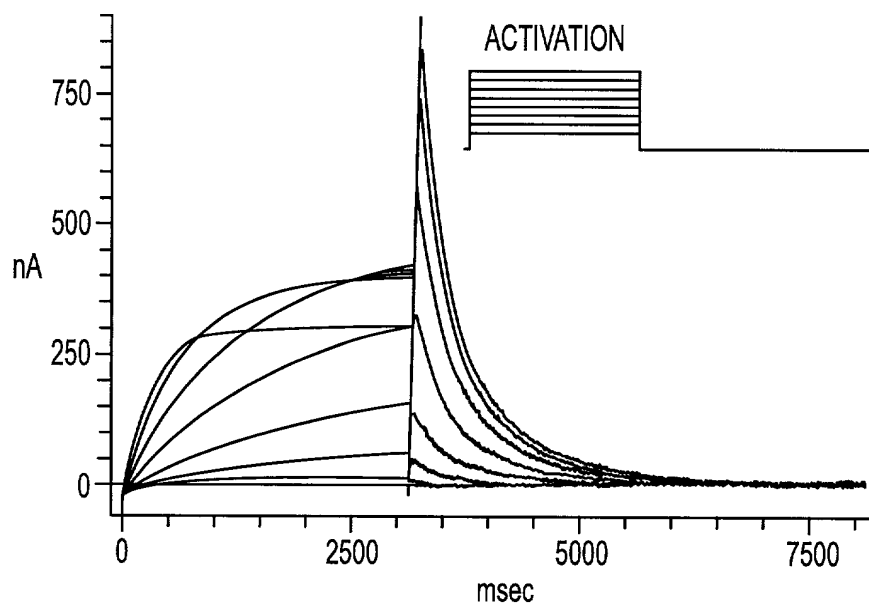


FIG. 2A

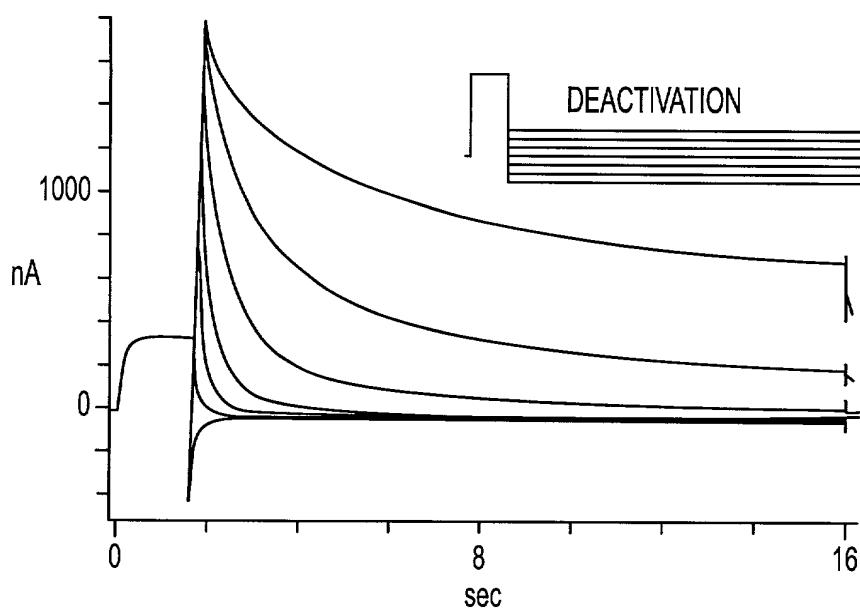


FIG. 2B

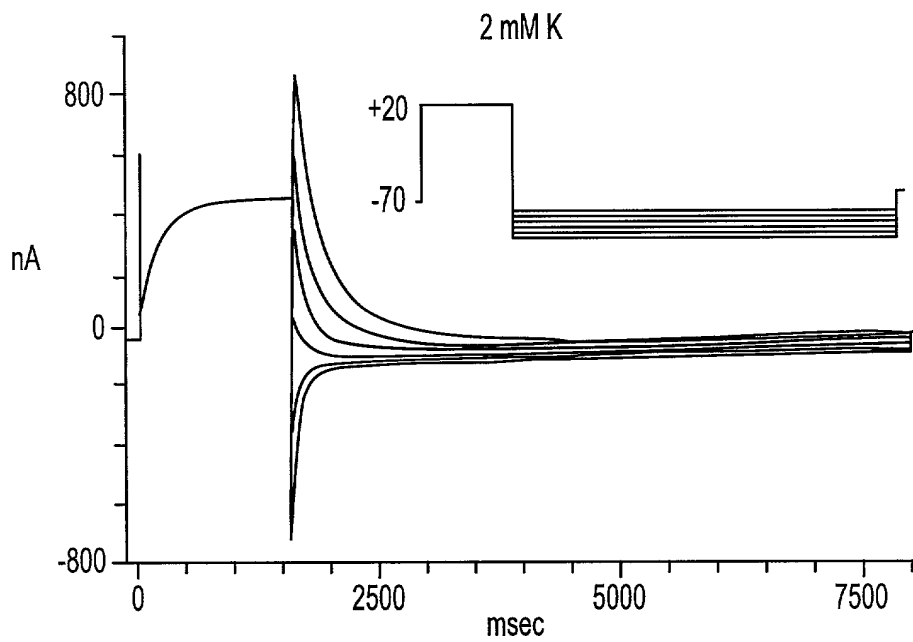


FIG. 3A

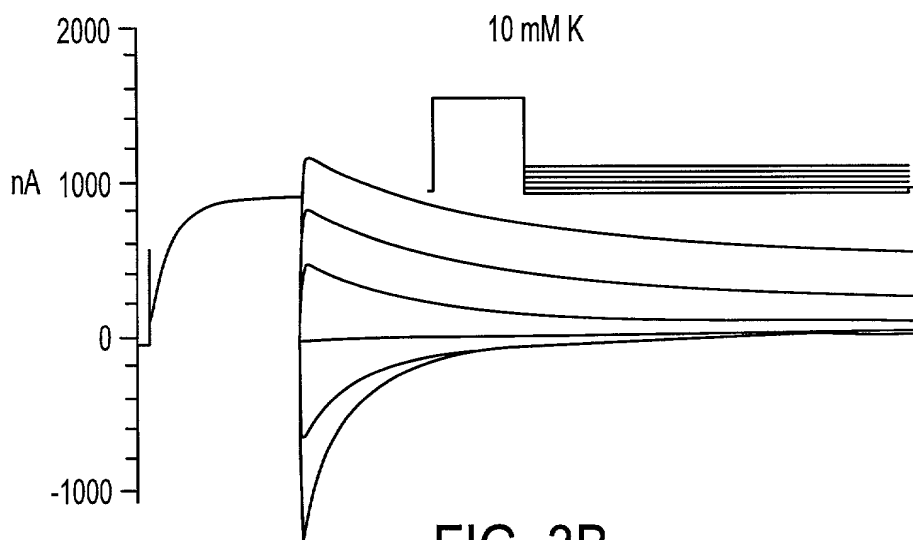


FIG. 3B

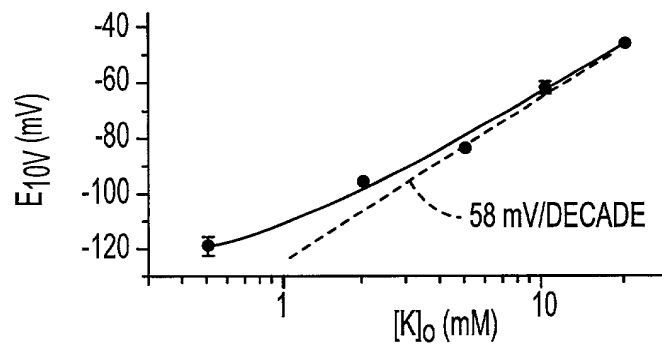


FIG. 3C

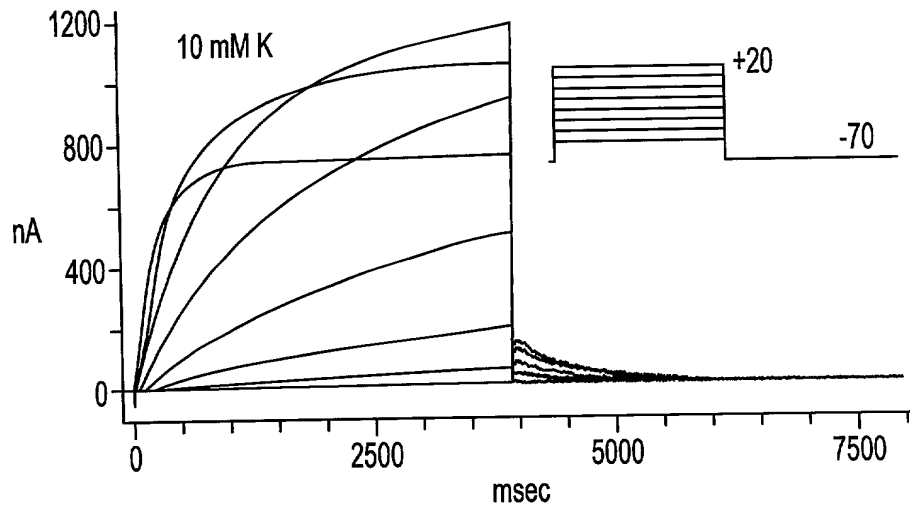


FIG. 4A

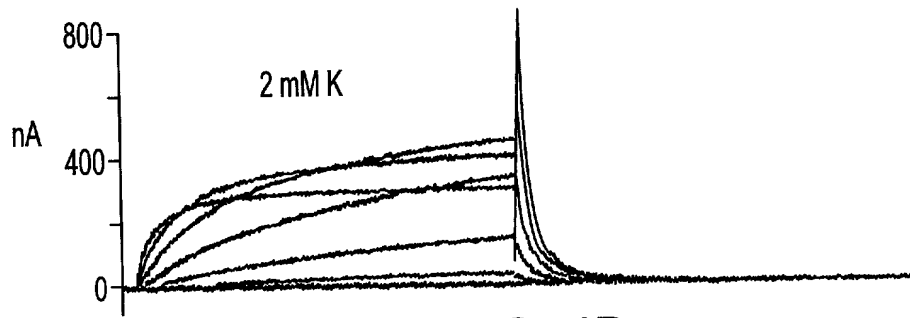


FIG. 4B

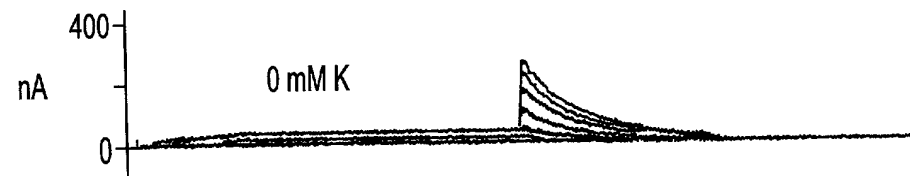


FIG. 4C

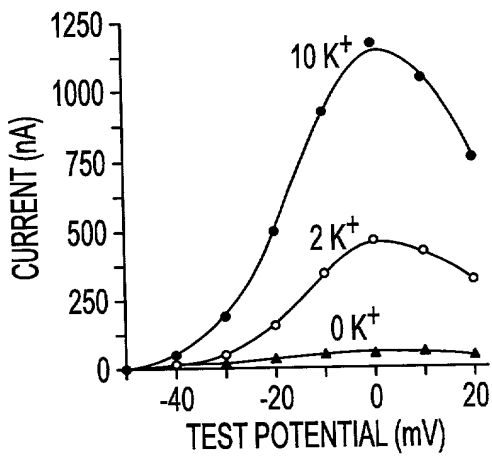


FIG. 4D

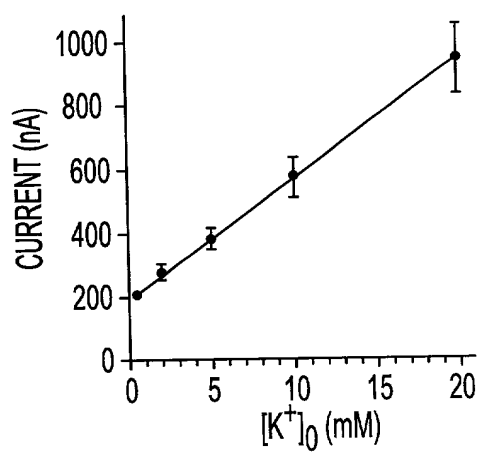


FIG. 4E

0073599-13400
004156656260

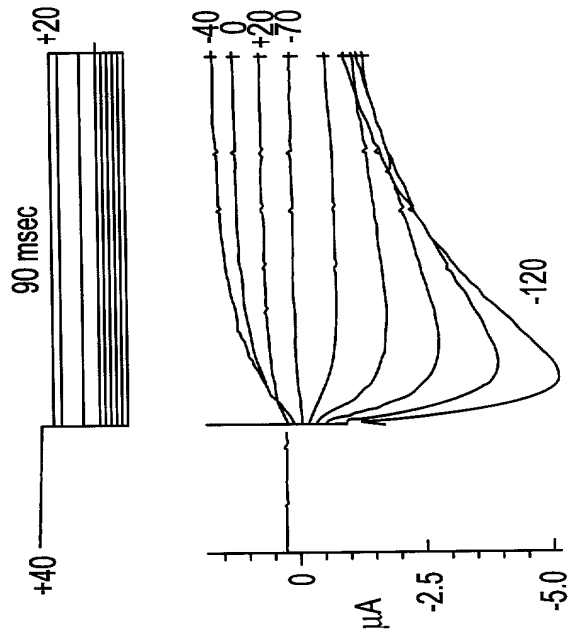


FIG. 5A

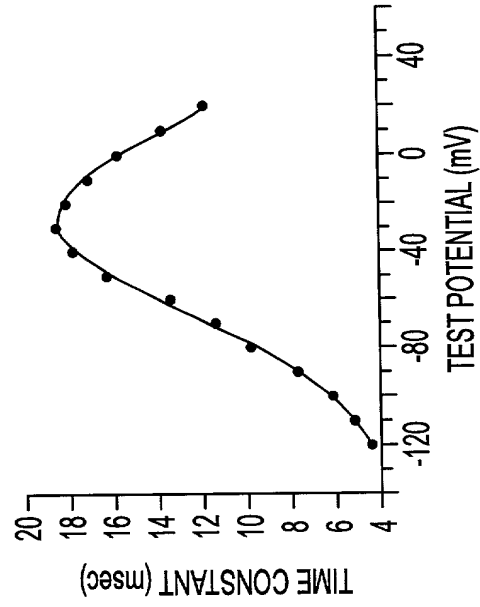
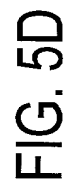
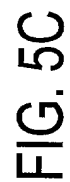


FIG. 5B



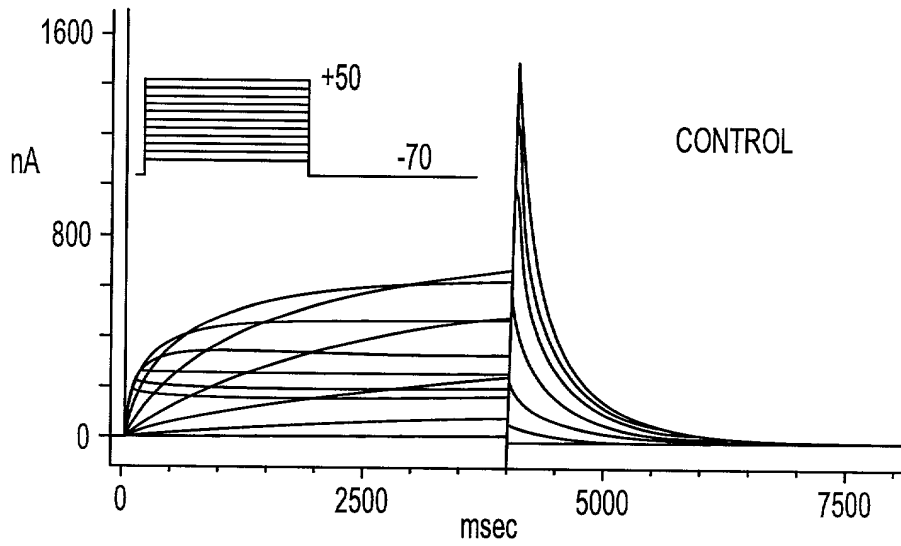


FIG. 6A

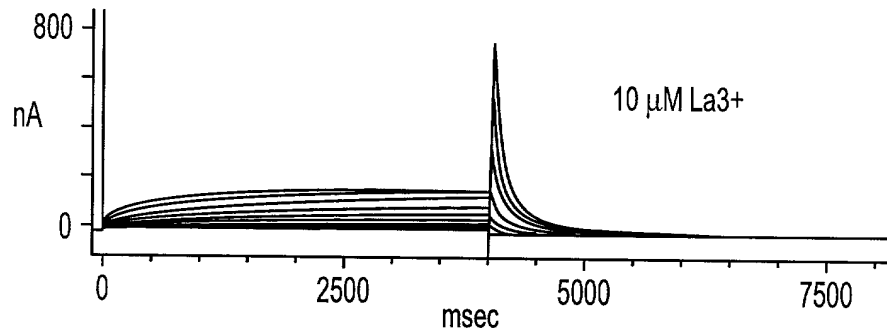


FIG. 6B

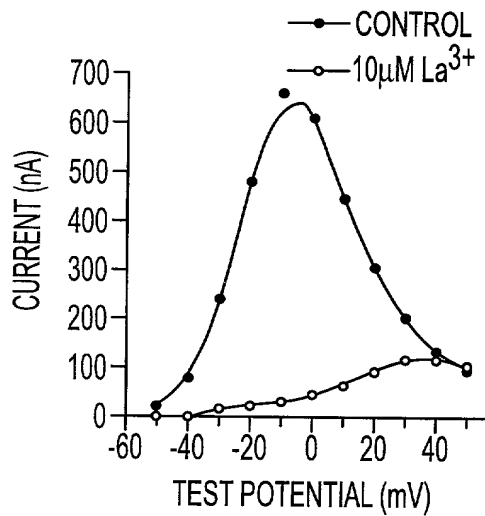


FIG. 6C

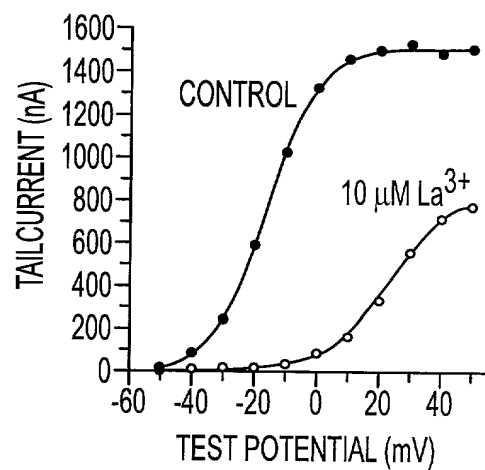


FIG. 6D

0073995-46656460

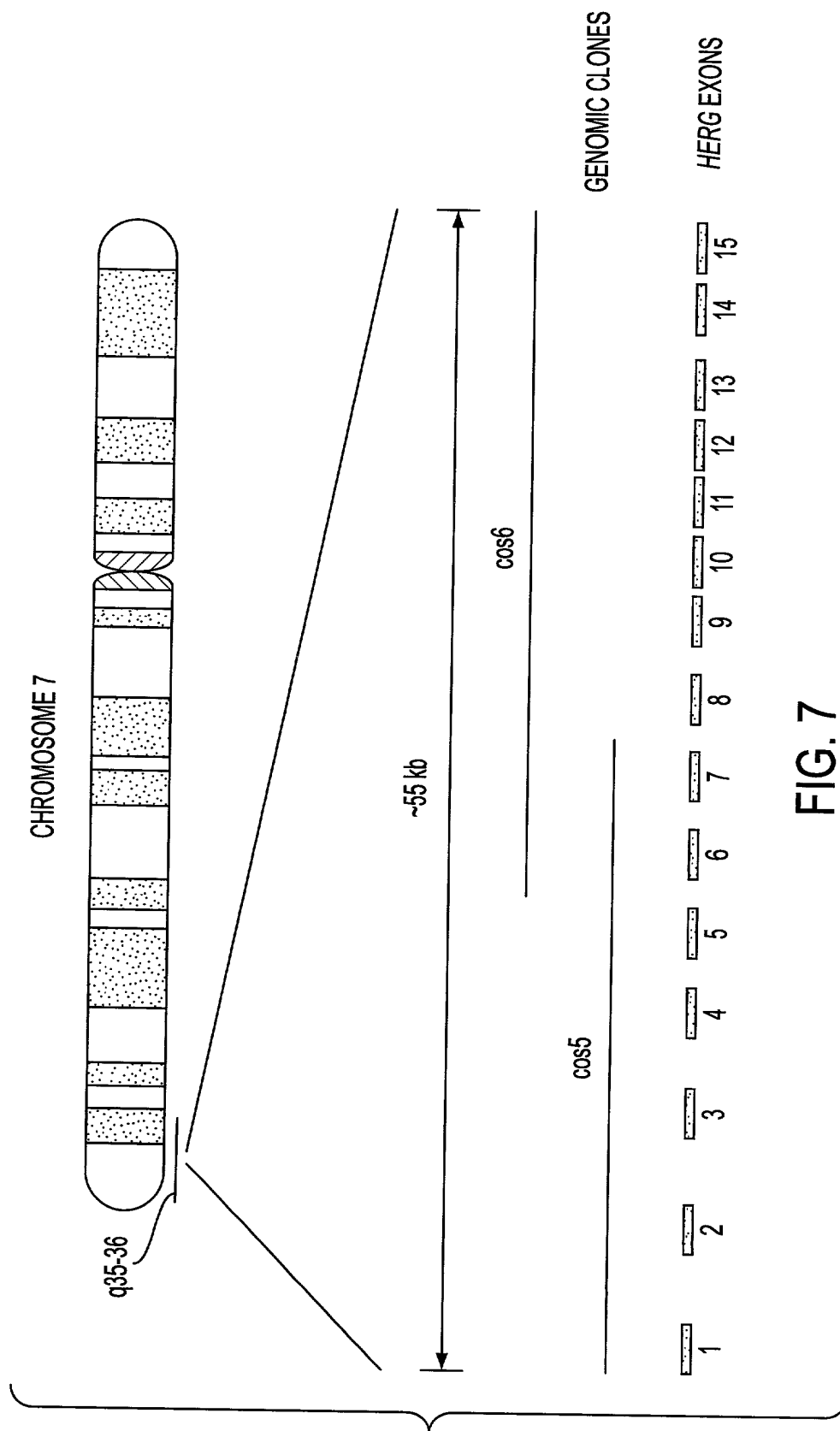


FIG. 7

AGCCTAGTGCTGGGCGGGCCGGGCGGGGTGGGTGGGGGCCCCCGGCCGCCCATGGGCTCAGGATGCCGGTGGCGAGG-81
GGCCACGTCGCGCCGAGAACACCTTCTGGACACCATCATCCGCAAGTTTGAGGGCCAGAGCCGTAAGTTCATCATCGCC-162
G H V A P O N T F L D T I I R K F E G O S R K F I I A -32
AACGCTCGGGTGGAGAACTGCGCCGTCTACTGCAACGACGGCTTCTGCGAGCTGTGCGGCTACTCGCGGGCCGAGGTG-243
N A R V E N C A V I Y C N D G F C E L C G Y S R A E V -59
ATGCAGCGACCCCTGCACCTGCGACTTCCTGCACGGGCCGCGCACGACGCGCGCTGCCGCGCAGATCGCGCAGGCACTG-324
M Q R P C T C D F L H G P R T Q R R A A A Q I A Q A L -86
CTGGCGCCGAGGAGCGCAAAGTGGAAATCGCCTTCTACCGAAAGATGGGAGCTGCTTCTATGTCTGGTGGATGTGGTG-405
L G A E E R K V E I A F F Y R K D G S C F L C L V D V V -113
CCCCGTAAGAACGAGGATGGGGCTGTTCATCATGTTCATCTCAATTTGAGGTGGTGTATGGAGAAGGACATGGTGGGGTCC-486
P V K N E D G A V I M F I L N F E V V M E K D M V G S -140
CCGGCTCATGACACCAACCACCGGGGCCCCCACCAGCTGGCTGGCCCCAGGCCGCGCAAGACCTTCCGCCTGAAGCTG-567
P A H D T N H R G P P T S W L A P G R A K T F R L K L -167
CCCCGCTGCTGGCGCTGACGGCCCGGAGTCGTCGGTGGCGTGGCGCGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGG-648
P A L L A L T A R E S S V R S G G A G G A G A P -194
GTGGTGGACGTGGACCTGACGCCCCGCGCACCCAGCAGCGAGTTCGCTGGCCCTGGACGAAGTGACAGCCATGGACACCAC-729
V V D V D L T P A A P S S E S L A L D E V T A M D N H -221
GTGGCAGGGCTCGGGCCCGGAGGAGCGGCGTGGCTGGTGGGTCCCGCTCTCCGCCCCGAGCGCGCGGGCCAGCTC-810
V A G L G P A E E R R A L V G P G S P P R S A P G Q L -248
CCATCGCCCCGGGCGCACAGCCTCAACCCCGACGCTCGGGCTCCAGCTGCAGCCTGGCCCGGACGCGCTCCCGAGAAAGC-891
P S P R A H S L N P D A S G S C S L A R T R S R E S -275
TGCGCCAGCGTGCAGCGCCCTCGTCGGCCGACGACATCGAGGCCATGCGCGCGGGGTGCTGCCCCCGCACCGCGCCAC-972
C A S V R R A S S A D D I E A M R A G V L P P P P R H -302
GCCAGCACCGGGCCATGCACCCACTGCGCAGCGGCTTGCTCAACTCCACCTCGGACTCCGACCTCGTGGCTACCGCACC-1053
A S T G A M H P L R S G L L N S T S D S D L V R Y R T -329
ATTAGCAAGATTCCCCAAATCACCTCAACTTTGTGGACCTCAAGGGCGACCCCTTCTTGGCTTCGCCACCAGTGACCGT-1134
I S K I P Q I T L N F V D L K G D P F L A S P T S D R -356
GAGATCATAGCACCTAAGATAAAGGAGCGAACCACAATGTCACTGAGAAGGTACCCAGGTCCTGTCCCTGGGCGCCGAC-1215
E I I A P K I K E R T H N V T E K V T Q V L S L G A D -383
GTGCTGCCTGAGTACAAGTGCAGGCACCGCGCATCCACCGCTGGACCATCCTGCATTACAGCCCCTCAAGGCCGTGTGG-1296
V L P E Y K L Q A P R I H R W T I L H Y S P F K A V W -410
GACTGGCTCATCTGCTGCTGGTCTATACACGGCTGTCTTACACCCCTACTCGGCTGCCTTCTGCTGAAGGAGACGGAA-1377
D W L I L L L V I Y T A V F T P Y S A A F L L K E T E -437
GAAGGCCCGCTGCTACCGAGTGTGGCTACGCCTGCCAGCGCTGGCTGTGGTGGACCTCATCGTGGACATCATGTTTCATT-1458
E G P P A T E C G Y A C Q P L A V V D L I V D I M F I -464
GTGGACATCCTCATCAACTTCCGCACCACTACGTCAATGCCAACGAGGAGGTGGTCAGCCACCCCGCGCATCGCCGTC-1539
V D I L I N F R T T Y V N A N E E V V S H P G R I A V -491
CACTACTTCAAGGGCTGGTTCTCATCGACATGGTGGCGCCATCCCTTTCGACCTGCTCATCTTTCGGCTCTGGCTCTGAG-1620
H Y F K G W F L I D M V A A I P F D L L I F G S G S E -518
GAGCTGATCGGGCTGCTGAAGACTGCGCGGCTGCTGCGGCTGGTGGCGGGAAGCTGGATCGCTACTCAGAGTAC-1701
E L I G L L K T A R L L R L V R V A R K L D R Y S E Y -545
GGCGCGCCGTGCTGTTCTTGCTCATGTGCACCTTTGCGCTCATCGCGCACTGGCTAGCCTGCATCTGGTACGCCATCGGC-1782
G A A V L F L L M C T F A L I A H W L A C I W Y A I G -572
AACATGGAGCAGCCACACATGGACTCAGCATCGGCTGGCTGCACAACCTGGGCGACCAGATAGGCAAACCTTACAACAGC-1863
N M E Q P H M D S R I G W L H N L G D Q I G K P Y N S -599
AGCGGCTGGGCGGCCCCCTCCATCAAGGACAAGTATGTGACGGCGCTTACTTACCTTACAGCAGCTCACCAGTGTGGGC-1944
S G L G G P S I K D K Y V T A L Y F T F S S L T S V G -626
TTCGGCAACGTCTCTCCCAACACCAACTCAGAGAAGATCTTCTCATCTGCGTCATGCTCATTTGGCTCCCTCATGTATGCT-2025
F G N V S P N T N S E K I F S I C V M L I G S L M Y A -653

FIG. 8A

AGCATCTTCGGCAACGTGTCGGCCATCATCCAGCGGCTGTACTCGGGCACAGCCCGCTACCACACACAGATGCTGCGGGTG-2106
S I F G N V S A I I O R L Y S G T A R Y H T Q M L R V -680

CGGGAGTTTCATCCGCTTCCACCAGATCCCCAATCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCACGCTGGTCTTAC-2187
R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707

▽

ACCAACGGCATCGACATGAACGCGGTGCTGAAGGGCTTCCTGAGTGCCTGCAGGCTGACATCTGCCTGCACCTGAACCGC-2268
T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734
TCACTGCTGCAGCACTGCAAACCTTCCGAGGGGCCACCAAGGGCTGCCTTCGGGGCCTGGCCATGAAGTTCAAGACCACA-2349
S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761
CATGCACCGCCAGGGGACACACTGGTGCATGCTGGGGACCTGCTCACC GCCCTGTACTTCATCTCCCGGGGCTCCATCGAG-2430
H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788

▽

ATCTGCGGGGCGACGTCGTCGTGGCCATCCTGGGGAAGAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511
I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815

cNBD

GGCAAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGTGGAGGTGCTG-2592
G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842

▽

GACATGTACCCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAACATGATCCCG-2673
D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869
GGCTCCCCCGGCAGTACGAGTTAGAGGGTGGCTTCACTCGGCAACGCAAGCGCAAGTTGTCTTCCGCAGGCGCACGGAC-2754
G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896

▽

AAGACACGGAGCAGCCAGGGGAGGTGTGCGCCTTGGGGCCGGCCGGGGCAGGGCCGAGTAGCCGGGGCCGGCCG-2835
K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923
GGGGGGCGTGGGGGAGAGCCCGTCCAGTGGCCCTCCAGCCCTGAGAGCAGTGAGGATGAGGGCCAGGCCGAGCTCC-2916
G G P W G E S P S S G P S S P E S S E D E G P G R S S -950
AGCCCCCTCCGCTGGTGGCTTCTCCAGCCCCAGCCCCCGGAGAGCCCGGGTGGGAGCCCTGATGGAGGACTGC-2997
S P L R L V P F S S P R P P G E P P G G E P L M E D C -977

▽

GAGAAGAGCAGCGACACTTGCAACCCCTGTGAGGCGCTTCTCAGGAGTGTCACATTTTCAGCTTCTGGGGGACAGT-3078
E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004
CGGGGCCCGCAGTACCAGGAGTCCCTCGATGCCCCGCCCCACCCAGCCTCCTCAACATCCCCCTCTCCAGCCCCGGT-3159
R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031

▽

CGCGGGCCCCGGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCA-3240
R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058
GACATGGCCACTGTCTGCAGTGCTACAGAGGCAGATGACGCTGGTCCCGCCCGCTACAGTGCTGTGACCACCCCGGG-3321
D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085

▽

CCTGGCCCCACTTCCACATCCCCGCTGTGCGCGTCAGCCCCCTCCCCACCTCACCTTGGA CTGCTTTCTCAGGTTTCC-3402
P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112
CAGTTTCATGGCGTGTGAGGAGCTGCCCCGGGGCCCCAGAGCTTCCCCAAGAAGGCCCCACACGACGCTCTCCCTACCG-3483
Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139
GGCCAGCTGGGGCCCTCACCTCCCAGCCCTGCACAGACACGGCTCGGACCCGGGCAGTTAGTGGGGCTGCCAGTGTGG-3564
G Q L G A L T S Q P L H R H G S D P G S * -1159
ACAGTGGCTCACCCAGGGATCAAGGCGCTGCTGGGCGCTCCCCTTGAGGCCCCTGCTCAGGAGGCCCTGACCGTGGAAG-3645
GGGAGAGGAAC TCGAAAGCACAGCTCTCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCCTGGGCCCCAGTGAGAG-3726
GGGCAGGGCAGGGCCGCGAGTAGGTGGGGCCTGTGGTCCCCCACTGCCCTGAGGGCATTAGCTGGTCTAACTGCCCGGA-3807
GGCACC CGCCCTGGGCCTTAGGCACCTCAAGGACTTTTCTGCTATTACTGCTCTATTGTTAAGGATAATAATTAAGGA-3888
TCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAATAATATCCTGAGGAG (A)_n -3949

FIG. 8B



00472-5665E2.60

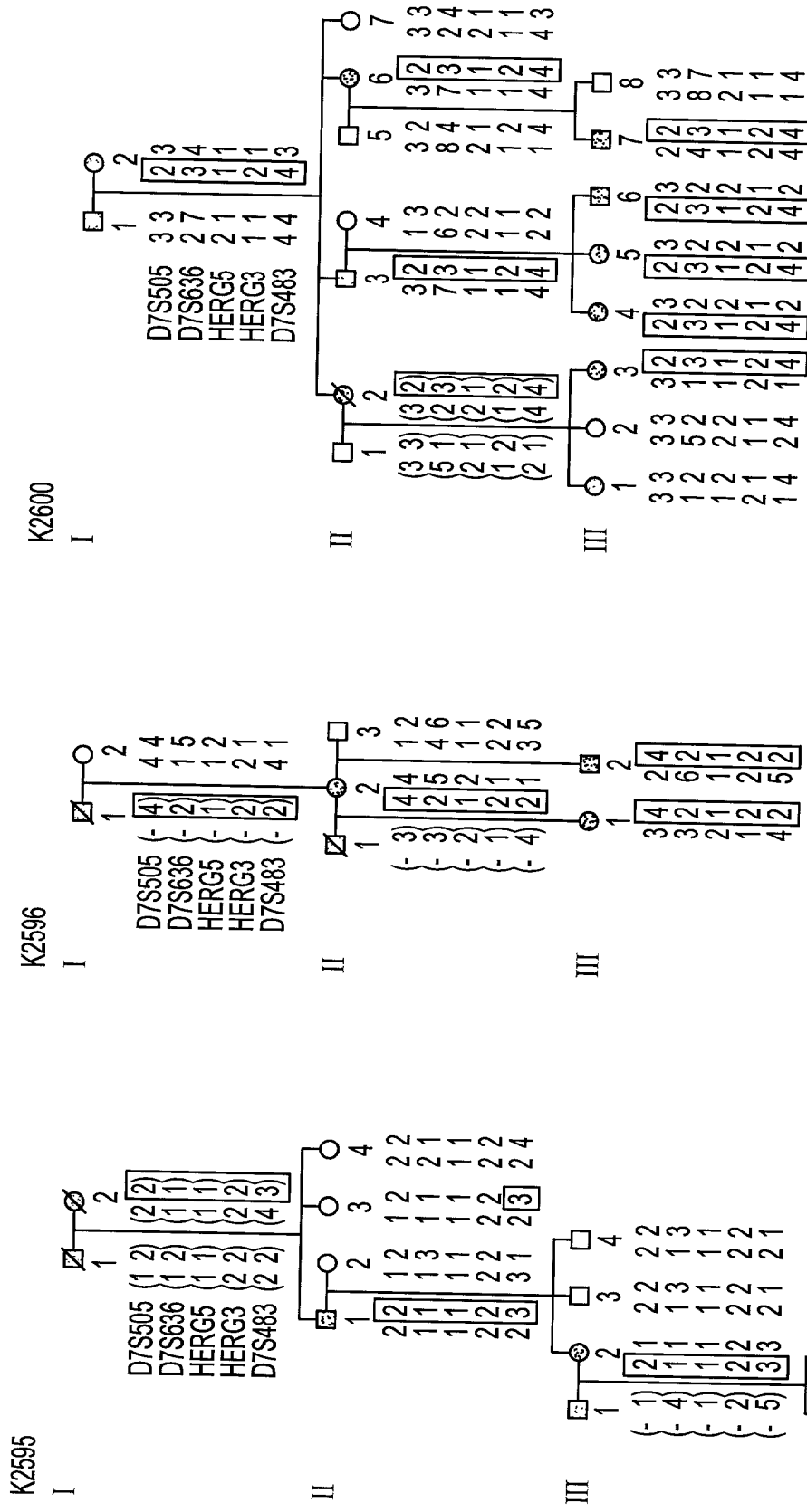


FIG. 9D

FIG. 9E

FIG. 9C

004767-5065E260

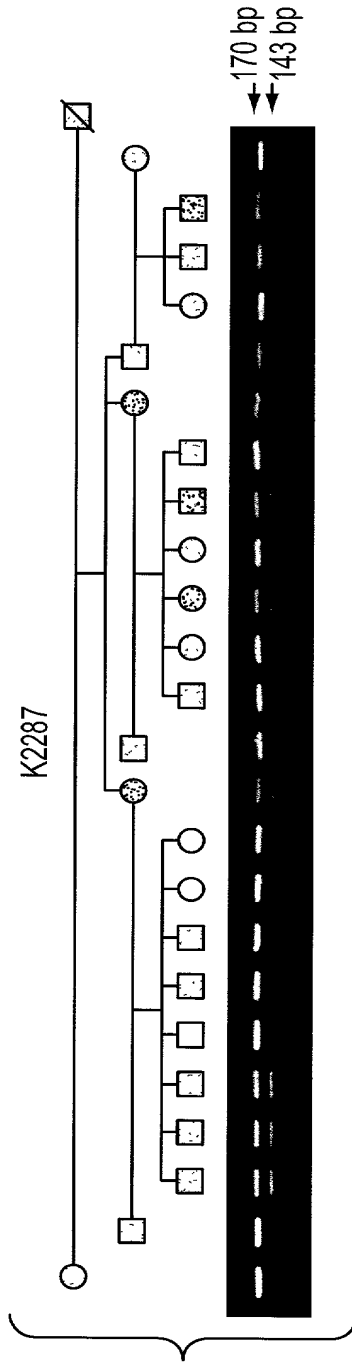


FIG. 10A

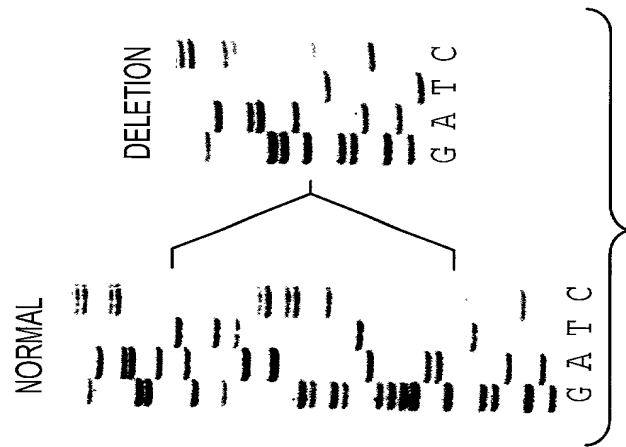


FIG. 10B

000127-56656/60

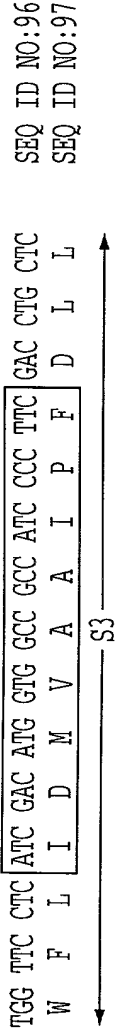
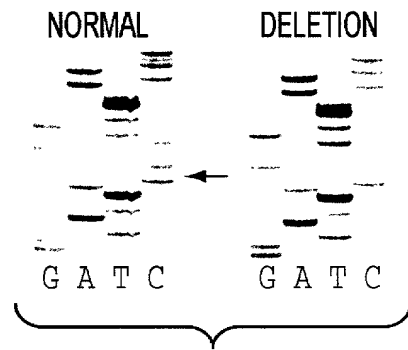
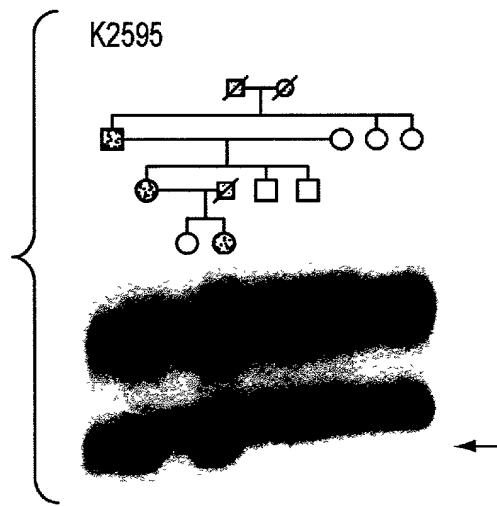


FIG. 10C

NORMAL	GTC ATC TAC ACG GCT GTC TTC ACA CCC TAC TCG GCT GCC TTC CTG CTG AAG GAG	SEQ ID NO:98
	V I Y T A V F T P Y S A A F L L K E	SEQ ID NO:99
DELETION	GTC ATC TAC CGG CTG TCT TCA CAC CCT ACT CGG CTG CCT TCC TGC TGA	SEQ ID NO:100
	V I Y R L S S S H P T R L P S C	SEQ ID NO:101

FIG. 11C



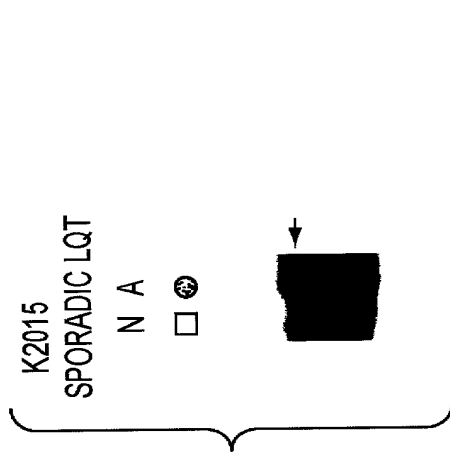


FIG. 12E

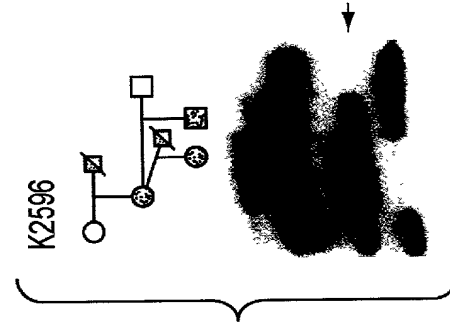


FIG. 12C

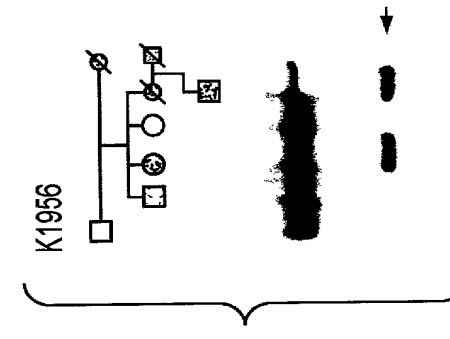


FIG. 12A

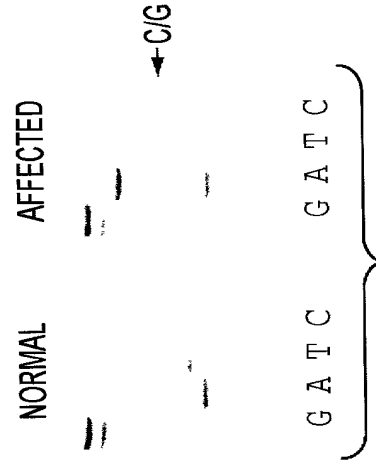


FIG. 12F

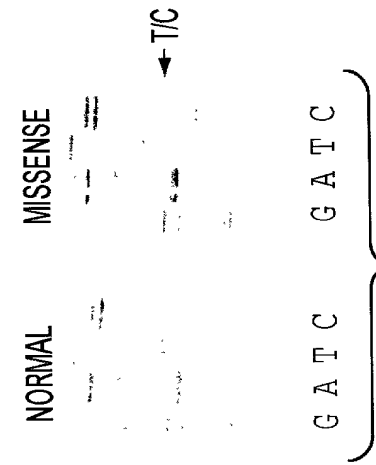


FIG. 12D

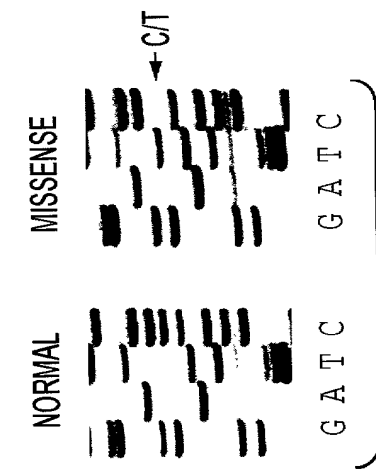


FIG. 12B

	GTG→V GCG \\	SEQ ID NO:
	L I A H W L ↔S5↔	102
K1956	L I V H W L	103
H-Erg	L I A H W L	102
M-Eag	L A A H W K	104
R-Eag	L A A H W M	105
Eag	L V A H W L	106
Elk	L A A H W L	107

FIG. 12G

	GAC→D AAC \\	SEQ ID NO:
	D I L I N F R ↔S2↔	108
K2596	D I L I D F R	109
H-Erg	D I L I N F R	108
M-Eag	D I V L N F H	110
R-Eag	D I V L N F H	110
Eag	D I V L N F H	110
Elk	D I L L N F R	111

FIG. 12H

5'-CAT CCT GG // gtatggg-3'
c ↓

FIG. 12I

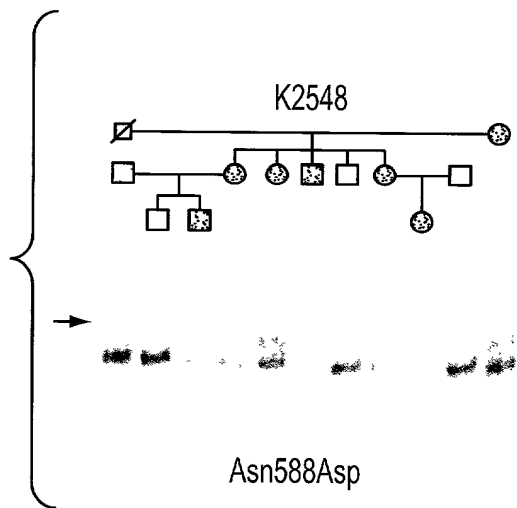


FIG. 13A



FIG. 13B

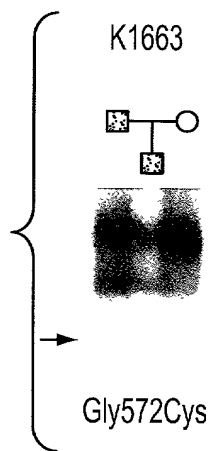


FIG. 13C

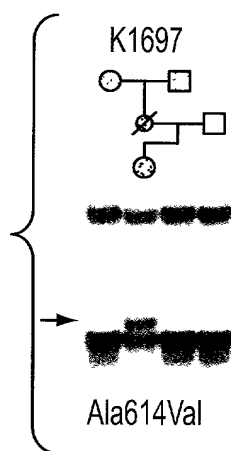


FIG. 13D

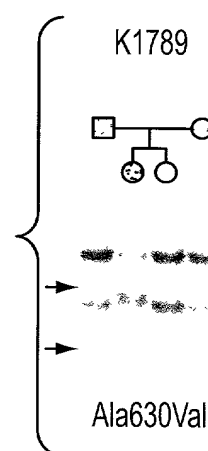


FIG. 13E

004727 50656260

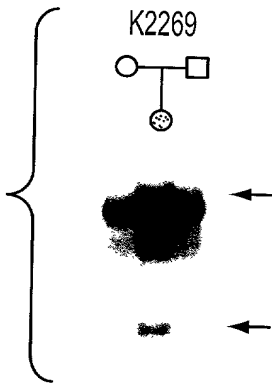


FIG. 14A

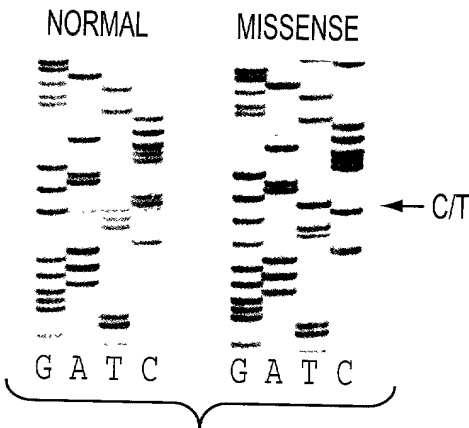


FIG. 14B

	AGC → S	SEQ ID
	GGC	NO:
	SVGFGNVS	112
	← PORE →	
K2269	SVGF SNVS	113
H-Erg	SVGFGNVS	112
M-Eag	SVGFGNIA	114
R-Eag	SVGFGNIA	114
Eag	SVGFGNVA	115
Elk	SVGFGNVS	112
Shaker	TVGYGDMT	116

FIG. 14C

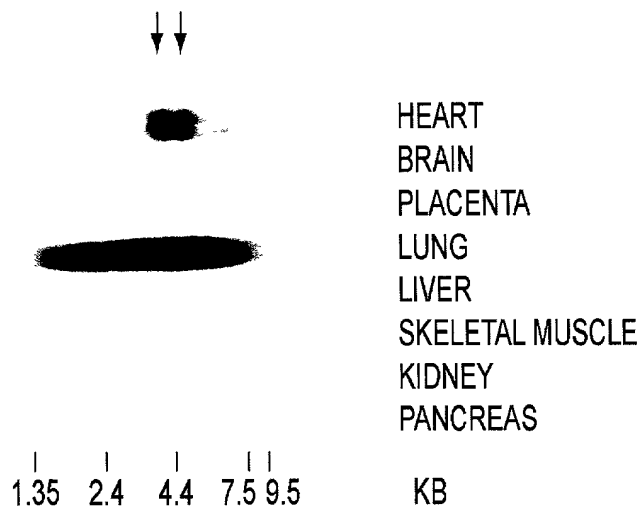


FIG. 15